

L2 ANSWER 1 OF 1 MEDLINE
AN 91209917 MEDLINE
DN 91209917
TI Glucosyltransferase gene polymorphism among *Streptococcus mutans* strains.
AU Chia J S; Hsu T Y; Teng L J; Chen J Y; Hahn L J; Yang C S
CS School of Dentistry, National Taiwan University, Taipei, Republic of China..
SO INFECTION AND IMMUNITY, (1991 May) 59 (5) 1656-60.
Journal code: G07. ISSN: 0019-9567.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199108
AB Genetic polymorphisms in genes coding for the glucosyltransferases were detected among *Streptococcus mutans* serotype c strains by Southern blot analysis with DNA probes located within the **gtfB gene** (H. Aoki, T. **Shiroza**, M. Hayakawa, S. Sato, and H. K. Kuramitsu, Infect. Immun. 53:587-594, 1986). Restriction endonucleases were used to examine genomic DNAs isolated from serotype a to h strains. The variations were readily detected among 33 strains of serotype c by EcoRI and PstI restriction enzyme digestions. Serotypes e and f, which are genetically similar to serotype c, also had comparable polymorphism; however, serotypes a, b, d, g, and h did not hybridize to the same DNA probes in parallel experiments. Further analysis of enzymatic activities for glucan synthesis and sucrose-dependent adherence revealed no significant differences among the serotype c strains. Our results suggested that genetic polymorphisms existing in *S. mutans* serotype c strains may reflect a complexity in genes coding for the glucosyltransferases, which are produc

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***** RPSrch_pp *****

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protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jan 11 15:47:50 2000;   MasPar time 2.45 Seconds
Output not generated.

Database: >USP09-290-049-3
Description: (1-22) from US0920049, pep
Perfect Score: 155
Sequence: TARTINGOLLYFRANGVQVK 22

Scoring table: PAM 150
Gap 15

Searched: 77977 seqs, 28268293 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot37
1.swissprot

Statistics:
Mean 29.681; Variance 38.978; scale 0.761

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

 8

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result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	155	100.0	1475	1	GTFB_STRU	GLUCOSYLTRANSFERASE-I	9.19e-23
2	114	73.5	1597	1	GTF1_STRUO	GLUCOSYLTRANSFERASE-I	4.74e-12
3	112	72.3	1592	1	GTF2_STRUO	GLUCOSYLTRANSFERASE-I	1.49e-11
4	106	68.4	1375	1	GTFC_STRU	GLUCOSYLTRANSFERASE-SI	4.46e-10
5	104	67.1	1365	1	GTFE_STRUO	GLUCOSYLTRANSFERASE-S	1.36e-09
6	93	60.0	1430	1	GTFD_STRU	GLUCOSYLTRANSFERASE-S	5.53e-07
7	79	51.0	382	1	YJ07_YEAST	HYPOTHETICAL	44.9 KD P
8	72	51.0	126	1	DOC_BPL1	DEATH ON CURING PROTEIN	7.50e-04
9	70	45.2	529	1	Y119_NPWP	HYPOTHETICAL	59.0 KD P
10	67	43.2	2710	1	TOXA_CLODI	TOXIN A.	2.19e-01
11	65	41.9	349	1	PTER_MOUSE	PHOSPHOTRIESTERASE REL	5.32e-01
12	65	41.9	1396	1	VLTB_BTG5	L-SHAPED TAIL FIRE PR	5.32e-01
13	63	40.6	301	1	LECI_MOUSE	ASIALOGLYCOPROTEIN REC	1.27e-00
14	63	40.6	310	1	YC08_PIRIO	HYPOTHETICAL SUGAR KIN	1.27e-00
15	63	40.6	349	1	PTER_RAT	PHOSPHOTRIESTERASE REL	1.27e+00
16	63	40.6	396	1	DUT_VVVD	DIXYURIDINE 5'-TRIPHO	1.27e+00
17	63	40.6	404	1	CAG5_CHICK	ALPHA-N-ACETYLGALACTOS	1.27e+00
18	63	40.6	475	1	AP54_YEAST	CLATHRIN COAT ASSEMBLY	1.27e+00
19	63	40.6	1082	1	RPP0_ROTPC	RNA-DIRECTED RNA POLY	1.27e+00
20	62	40.6	464	1	VL2_HPV2	MINOR CAPSID PROTEIN L	1.95e+00
21	62	40.6	467	1	ISP6_SCHPO	SEXUAL DIFFERENTIATION	1.95e+00
22	62	40.6	524	1	VL2 HPV2A	MINOR CAPSID PROTEIN L	1.95e+00
23	64	40.6	1076	1	VNP16	TOPBP1	2.07e+00

ALIGNMENTS

FT CHAIN 35 1475 GLUCOSYLTRANSFERASE-I; CATALYTIC (APPROXIMATE).
 FT DOMAIN 35 1050 GLUCAN-BINDING (APPROXIMATE).
 FT REPEAT 1096 1475 A REPEAT.
 FT DOMAIN 1160 1469 5 X TANDEM REPEATS.
 FT REPEAT 1160 1209 1.
 FT REPEAT 1224 1274 2.
 FT REPEAT 1289 1339 3.
 FT REPEAT 1354 1404 4.
 FT REPEAT 1419 1469 5.
 SO SEQUENCE 1475 AA; 165812 MW; 4542C1D6 CRC32;

Query Match 100.0%; Score 155; DB 1; Length 1475;
 Best Local Similarity 100.0%; Pred. No. 9.19e-23;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 TGARTINGOLLYFRANGVQVKG 22

RESULT 2
 ID GTF1_STRDO STANDARD; PRT; 1597 AA.
 AC P27410;
 DT 1-JUL-1989 (REL. 11, CREATED)
 DT 01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE GLUCOSYLTTRANSFERASE-I PRECURSOR (EC 2.4.1.5) (GTF-1) (DEXTRANSUCRASE)
 DE (SUCROSE 6-GLUCOSYLTRANSFERASE).
 GN GTF1.
 OS STREPTOCOCCUS DOWNEI (STREPTOCOCCUS SOBRINUS).
 OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
 OC STREPTOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MFE28;
 RX MEDLINE: 87308014.
 RA FERRETTI J.J., GILIN M.L., RUSSELL R.R.B.;
 RT Nucleotide sequence of a glucosyltransferase gene from Streptococcus
 RT subsp. MFE28.;
 RL J. BACTERIOL. 169:4271-4278(1987).
 CC -I- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
 TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE
 OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE
 AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.
 CC -I- CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) - D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).
 CC -I- SUBCELLULAR LOCATION: SECRETED.
 CC -I- DISEASE: DENTAL CARIES.
 CC -I- GTF-1 SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED
 GLUCOSE AND SOME 1,6 LINKAGES). GTF-SI SYNTHESIZES WATER-SOLUBLE
 GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH FORMS OF
 CC -I- SIMILARITY: TO OTHER GLUCOSYLTTRANSFERASES AND SOME TO A GLUCAN-
 CC BINDING PROTEIN FROM S. MUTANS.

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 CC
 DR EMBL: M17391; G153647;
 DR PFAM: PF00128; alpha-amylase; 1.
 KW TRANSFERASE; GLYCOSYLTTRANSFERASE; SIGNAL; REPEAT; DENTAL CARIES.
 FT SIGNAL 1 38 POTENTIAL.
 FT CHAIN 39 1597 GLYCOSYLTTRANSFERASE-I.
 FT DOMAIN 39 1050 CATALYTIC (APPROXIMATE).
 FT DOMAIN 1099 1597 GLUCAN-BINDING (APPROXIMATE).
 FT DOMAIN 1099 1597 1.25 A, 2 B, AND 5 AC REPEATS.
 FT REPEAT 1099 1132 A REPEAT.

FT REPEAT 1163 1213 AC REPEAT.
 FT REPEAT 1227 1277 AC REPEAT.
 FT REPEAT 1292 1342 AC REPEAT.
 FT REPEAT 1352 1399 B REPEAT.
 FT REPEAT 1406 1455 AC REPEAT.
 FT REPEAT 1465 1512 B REPEAT.
 FT REPEAT 1519 1568 AC REPEAT.
 FT REPEAT 1582 1597 A REPEAT (INCOMPLETE).

SO SEQUENCE 1597 AA; 177080 MW; 995233CA CRC32;

Query Match 73.5%; Score 114; DB 1; Length 1597;
 Best Local Similarity 77.3%; Pred. No. 4.74e-12;
 Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 TGARTINGOLLYFRANGVQVKG 22

RESULT 3
 ID GTF2_STRDO STANDARD; PRT; 1592 AA.
 AC P27410;
 DT 01-AUG-1992 (REL. 23, CREATED)
 DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE GLUCOSYLTTRANSFERASE-I PRECURSOR (EC 2.4.1.5) (GTF-1) (DEXTRANSUCRASE)
 DE (SUCROSE 6-GLUCOSYLTRANSFERASE).
 OS STREPTOCOCCUS DOWNEI (STREPTOCOCCUS SOBRINUS).
 OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MFE28;
 RX MEDLINE: 9113227.
 RA ABO H., MATSUMURA T., OHTA H., FUKUI K., KATO K.,
 RA KAWARA H.,
 RT "Peptide sequences for sucrose splitting and glucan binding within
 Streptococcus sobrinus glucosyltransferase (water-insoluble glucan
 synthetase)", J. BACTERIOL. 173:989-996(1991).
 RL CC -I- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
 TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE
 OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE
 AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.
 CC -I- CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) - D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).
 CC -I- SUBCELLULAR LOCATION: SECRETED.
 CC -I- DISEASE: DENTAL CARIES.
 CC -I- GTF-1 SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED
 GLUCOSE AND SOME 1,6 LINKAGES). GTF-SI SYNTHESIZES WATER-SOLUBLE
 GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH FORMS OF
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 CC
 DR EMBL: D99213; G217033; -.
 DR PIR: A38175; A38175.
 DR PFAM: PF00128; alpha-amylase; 1.
 DR HSSP: P00695; ZHEE.
 KW TRANSFERASE; GLYCOSYLTTRANSFERASE; SIGNAL; REPEAT; DENTAL CARIES.
 FT SIGNAL 1 38 POTENTIAL.
 FT CHAIN 39 1592 CATALYTIC (APPROXIMATE).
 FT DOMAIN 39 1044 GLUCAN-BINDING (APPROXIMATE).
 FT DOMAIN 1093 1592 6.5 X TANDEM REPEATS.